

FIGURE 1

(Seq ID NO:36)
 GAGCTCGGAT CCACTACTCG ACCCACGCGT CCGGCCAGGA CCTCTGTGAA CCGGTCGGGG 60
 CGGGGGCCGC CTGGCCGGGA GTCTGCTCGG CCGTGGGTGG CCGAGGAAGG GAGAGAACGA 120
 TCGCGGAGCA GGGCGCCCGA ACTCCGGGCG CCGCGCC ATG CGC CGG GCC AGC CGA 175
 (Seq ID NO:37) Met Arg Arg Ala Ser Arg
 1 5
 GAC TAC GGC AAG TAC CTG CGC AGC TCG GAG GAG ATG GGC AGC GGC CCC 223
 Asp Tyr Gly Lys Tyr Leu Arg Ser Ser Glu Glu Met Gly Ser Gly Pro
 10 15 20
 GGC GTC CCA CAC GAG GGT CCG CTG CAC CCC GCG CCT TCT GCA CCG GCT 271
 Gly Val Pro His Glu Gly Pro Leu His Pro Ala Pro Ser Ala Pro Ala
 25 30 35
 CCG GCG CCG CCA CCC GCC GCC TCC CGC TCC ATG TTC CTG GCC CTC CTG 319
 Pro Ala Pro Pro Pro Ala Ala Ser Arg Ser Met Phe Leu Ala Leu Leu
 40 45 50
 GGG CTG GGA CTG GGC CAG GTG GTC TGC AGC ATC GCT CTG TTC CTG TAC 367
Gly Leu Gly Leu Gly Gln Val Val Cys Ser Ile Ala Leu Phe Leu Tyr
 55 60 65 70
 TTT CGA GCG CAG ATG GAT CCT AAC AGA ATA TCA GAA GAC AGC ACT CAC 415
 Phe Arg Ala Gln Met Asp Pro Asn Arg Ile Ser Glu Asp Ser Thr His
 75 80 85
 TGC TTT TAT AGA ATC CTG AGA CTC CAT GAA AAC GCA GGT TTG CAG GAC 463
 Cys Phe Tyr Arg Ile Leu Arg Leu His Glu Asn Ala Gly Leu Gln Asp
 90 95 100
 TCG ACT CTG GAG AGT GAA GAC ACA CTA CCT GAC TCC TGC AGG AGG ATG 511
 Ser Thr Leu Glu Ser Glu Asp Thr Leu Pro Asp Ser Cys Arg Arg Met
 105 110 115
 AAA CAA GCC TTT CAG GGG GCC GTG CAG AAG GAA CTG CAA CAC ATT GTG 559
 Lys Gln Ala Phe Gln Gly Ala Val Gln Lys Glu Leu Gln His Ile Val
 120 125 130
 GGG CCA CAG CGC TTC TCA GGA GCT CCA GCT ATG ATG GAA GGC TCA TGG 607
 Gly Pro Gln Arg Phe Ser Gly Ala Pro Ala Met Met Glu Gly Ser Trp
 135 140 145 150
 TTG GAT GTG GCC CAG CGA GGC AAG CCT GAG GCC CAG CCA TTT GCA CAC 655
 Leu Asp Val Ala Gln Arg Gly Lys Pro Glu Ala Gln Pro Phe Ala His
 155 160 165
 CTC ACC ATC AAT GCT GCC AGC ATC CCA TCG GGT TCC CAT AAA GTC ACT 703
 Leu Thr Ile Asn Ala Ala Ser Ile Pro Ser Gly Ser His Lys Val Thr
 170 175 180

Sequence

FIGURE 1 (Con't)

CTG TCC TCT TGG TAC CAC GAT CGA GGC TGG GCC AAG ATC TCT AAC ATG	751
Leu Ser Ser Trp Tyr His Asp Arg Gly Trp Ala Lys Ile Ser <u>Asn</u> Met	
185 190 195	
ACG TTA AGC AAC GGA AAA CTA AGG GTT AAC CAA GAT GGC TTC TAT TAC	799
Thr Leu Ser Asn Gly Lys Leu Arg Val Asn Gln Asp Gly Phe Tyr Tyr	
200 205 210	
CTG TAC GCC AAC ATT TGC TTT CGG CAT CAT GAA ACA TCG GGA AGC GTA	847
Leu Tyr Ala Asn Ile Cys Phe Arg His His Glu Thr Ser Gly Ser Val	
215 220 225 230	
CCT ACA GAC TAT CTT CAG CTG ATG GTG TAT GTC GTT AAA ACC AGC ATC	895
Pro Thr Asp Tyr Leu Gln Leu Met Val Tyr Val Val Lys Thr Ser Ile	
235 240 245	
AAA ATC CCA AGT TCT CAT AAC CTG ATG AAA GGA GGG AGC ACG AAA AAC	943
Lys Ile Pro Ser Ser His Asn Leu Met Lys Gly Gly Ser Thr Lys <u>Asn</u>	
250 255 260	
TGG TCG GGC AAT TCT GAA TTC CAC TTT TAT TCC ATA AAT GTT GGG GGA	991
Trp Ser Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly	
265 270 275	
TTT TTC AAG CTC CGA GCT GGT GAA GAA ATT AGC ATT CAG GTG TCC AAC	1039
Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile Ser Ile Gln Val Ser <u>Asn</u>	
280 285 290	
CCT TCC CTG CTG GAT CCG GAT CAA GAT GCG ACG TAC TTT GGG GCT TTC	1087
Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe	
295 300 305 310	
AAA GTT CAG GAC ATA GAC T GAGACTCAT TCGTGGAACA TTAGCATGGA	1136
Lys Val Gln Asp Ile Asp	
315	
TGTCCTAGAT GTTTGGAAAC TTCTTAAAAA ATGGATGATG TCTATACATG TGTAAGACTA	1196
CTAAGAGACA TGGCCCACGG TGTATGAAAC TCACAGCCCT CTCTCTTGAG CCTGTACAGG	1256
TTGTGTATAT GTAAAGTCCA TAGGTGATGT TAGATTTCATG GTGATTACAC AACGGTTTTA	1316
CAATTTTGTA ATGATTTCCCT AGAATTGAAC CAGATTGGGA GAGGTATTCC GATGCTTATG	1376
AAAACTTAC ACGTGAGCTA TGGAAGGGGG TCACAGTCTC TGGGTCTAAC CCCTGGACAT	1436
GTGCCACTGA GAACCTTGAA ATTAAGAGGA TGCCATGTCA TTGCAAAGAA ATGATAGTGT	1496
GAAGGGTTAA GTTCTTTTGA ATTGTTACAT TGCGCTGGGA CCTGCAAATA AGTTCTTTTT	1556

FIGURE 1 (Con't)

TTCTAATGAG	GAGAGAAAAA	TATATGTATT	TTTATATAAT	GTCTAAAGTT	ATATTTTCAGG	1616
TGTAATGTTT	TCTGTGCAAA	GTTTTGTAAA	TTATATTTGT	GCTATAGTAT	TTGATTCAAA	1676
ATATTTAAAA	ATGTCTCACT	GTTGACATAT	TTAATGTTTT	AAATGTACAG	ATGTATTTAA	1736
CTGGTGCACT	TTGTAATTCC	CCTGAAGGTA	CTCGTAGCTA	AGGGGGCAGA	ATACTGTTTC	1796
TGGTGACCAC	ATGTAGTTTA	TTTCTTTATT	CTTTTAACT	TAATAGAGTC	TTCAGACTTG	1856
TCAAACTAT	GCAAGCAAAA	TAAATAAATA	AAAATAAAAT	GAATACCTTG	AATAATAAGT	1916
AGGATGTTGG	TCACCAGGTG	CCTTTCAAAT	TTAGAAGCTA	ATTGACTTTA	GGAGCTGACA	1976
TAGCCAAAAA	GGATACATAA	TAGGCTACTG	AAATCTGTCA	GGAGTATTTA	TGCAATTATT	2036
GAACAGGTGT	CTTTTTTTAC	AAGAGCTACA	AATTGTAAAT	TTTGTTTCTT	TTTTTTCCCA	2096
TAGAAAATGT	ACTATAGTTT	ATCAGCCAAA	AAACAATCCA	CTTTTAAATT	TAGTGAAAGT	2156
TATTTTATTA	TACTGTACAA	TAAAAGCATT	GTCTCTGAAT	GTTAATTTTT	TGGTACAAAA	2216
AATAAATTTG	TACGAAAACC	TGAAAAAAA	AAAAAAAAA	AAAAAAGGG	CGGCCGCTCT	2276
AGAGGGCCCT	ATTCTATAG					2295

Expression of 32D-F3 in COS-7 Cells

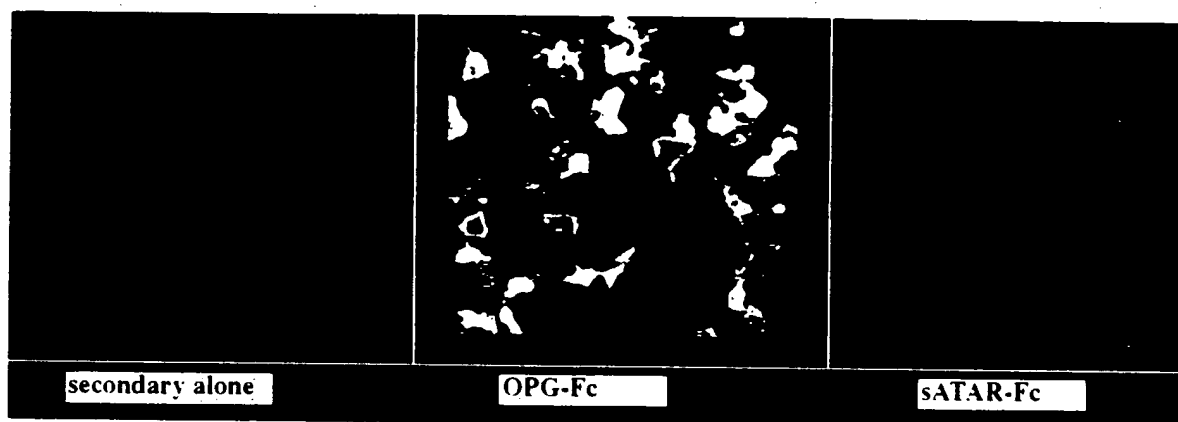


FIGURE 2

OPG Binding Protein Expression in Human Tissues

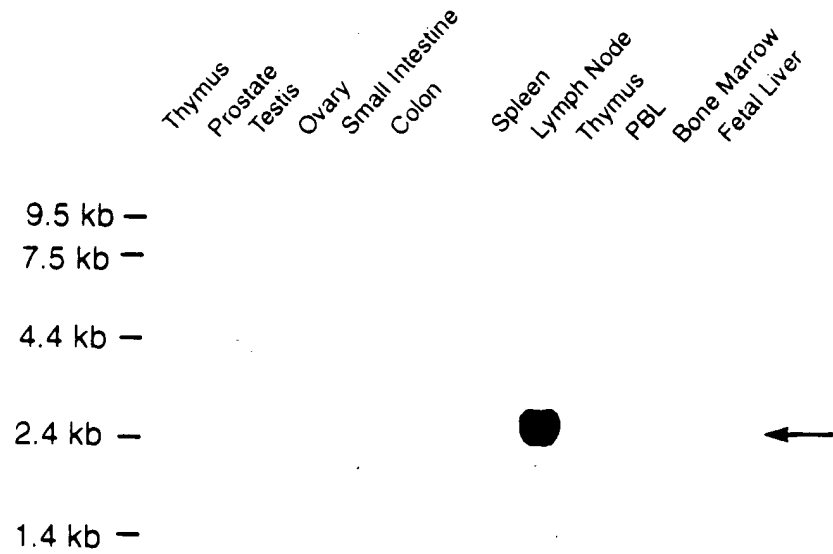


FIGURE 3

FIGURE 4

B (Seq ID No: 38)

10 30 50
AAGCTTGGTACCGAGCTCGGATCCACTACTCGACCCACGCGTCCGCGCGCCCCAGGAGCC

70 90 110
AAAGCCGGGCTCCAAGTCGGCGCCCCACGTCGAGGCTCCGCCGCAGCCTCCGGAGTTGGC

130 150 170
CGCAGACAAGAAGGGGAGGGAGCGGGAGAGGGAGGAGAGCTCCGAAGCGAGAGGGCCGAG

190 210 230
CGCCATGCGCCGCGCCAGCAGAGACTACACCAAGTACCTGCGTGGCTCGGAGGAGATGGG

B (Seq ID No: 39) M R R A S R D Y T K Y L R G S E E M G

250 270 290
CGGCGGCCCCGGAGCCCCGCACGAGGGCCCCCTGCACGCCCCGCCGCCCTGCGCCGCA
G G P G A P H E G P L H A P P P P A P H

310 330 350
CCAGCCCCCGCCGCTCCCGCTCCATGTTCTGCGGCCCTCCTGGGGCTGGGGCTGGGCCA
Q P P A A S R S M F V A L L G L G L G Q

370 390 410
GGTTGTCTGCAGCGTCGCCCTGTTCTTCTATTTTCAGAGCGCAGATGGATCCTAATAGAAT
V V C S V A L F F Y F R A Q M D P N R I

430 450 470
ATCAGAAGATGGCACTCACTGCATTTATAGAATTTTGAGACTCCATGAAAATGCAGATTT
S E D G T H C I Y R I L R L H E N A D F

490 510 530
TCAAGACACAACCTCTGGAGAGTCAAGATACAAAATTAATACCTGATTTCATGTAGGAGAAT
Q D T T L E S Q D T K L I P D S C R R I

550 570 590
TAAACAGGCCTTTCAAGGAGCTGTGCAAAAGGAATTACAACATATCGTTGGATCACAGCA
K Q A F Q G A V Q K E L Q H I V G S Q H

610 630 650
CATCAGAGCAGAGAAAGCGATGGTGGATGGCTCATGGTTAGATCTGGCCAAGAGGAGCAA
I R A E K A M V D G S W L D L A K R S K

670 690 710
GCTTGAAGCTCAGCCTTTTGCTCATCTCACTATTAATGCCACCGACATCCCATCTGGTTC
L E A Q P F A H L T I N A T D I P S G S

730 750 770
CCATAAAGTGAGTCTGTCCTCTTGGTACCATGATCGGGGTGGGCCAAGATCTCCAACAT
H K V S L S S W Y H D R G W A K I S N M

790 810 830
GACTTTTAGCAATGGAAAACCTAATAGTTAATCAGGATGGCTTTTATTACCTGTATGCCAA
T F S N G K L I V N Q D G F Y Y L Y A N

850 870 890
CATTTGCTTTTCGACATCATGAACTTCAGGAGACCTAGCTACAGAGTATCTTCAACTAAT
I C F R H H E T S G D L A T E Y L Q L M

910 930 950
GGTGTACGTCACTAAAACCAGCATCAAAATCCCAAGTTCTCATACCCTGATGAAAGGAGG
V Y V T K T S I K I P S S H T L M K G G

970 990 1010

GenBank

FIGURE 4

AAGCACCAAGTATTGGTCAGGGAATTCTGAATTCATTTTTATTCCATAAACGTTGGTGG
 S T K Y W S G N S E F H F Y S I N V G G
 1030 1050 1070
 ATTTTTTAAGTTACGGTCTGGAGAGGAAATCAGCATCGAGGTCTCCAACCCCTCCTTACT
 F F K L R S G E E I S I E V S N P S L L
 1090 1110 1130
 GGATCCGGATCAGGATGCAACATACTTTGGGGCTTTTAAAGTTTCGAGATATAGATTGAGC
 D P D Q D A T Y F G A F K V R D I D
 1150 1170 1190
 CCCAGTTTTTGGAGTGTATGTATTTCCCTGGATGTTTGGAAACATTTTTTAAACAAGCC
 1210 1230 1250
 AAGAAAGATGTATATAGGTGTGTGAGACTACTAAGAGGCATGGCCCCAACGGTACACGAC
 1270 1290 1310
 TCAGTATCCATGCTCTTGACCTTGTAGAGAACACGCGTATTTACAGCCAGTGGGAGATGT
 1330 1350 1370
 TAGACTCATGGTGTGTTACACAATGGTTTTTAAATTTTGTAAATGAATTCCTAGAAATTA
 1390 1410 1430
 CCAGATTGGAGCAATTACGGGTGACCTTATGAGAACTGCATGTGGGCTATGGGAGGGG
 1450 1470 1490
 TTGGTCCCCTGGTCATGTGCCCCCTTCGCAGCTGAAGTGGAGAGGGTGTCTATCTAGCGCAAT
 1510 1530 1550
 TGAAGGATCATCTGAAGGGGCAAATTCCTTTTGAATTGTTACATCATGCTGGAACCTGCAA
 1570 1590 1610
 AAAAATACTTTTTCTAATGAGGAGAGAAAATATATGTATTTTTTATATAATATCTAAAGTTA
 1630 1650 1670
 TATTTTCAGATGTAATGTTTTCTTTGCAAAGTATTGTAAATTATATTTGTGCTATAGTATT
 1690 1710 1730
 TGATTCAAAATATTTAAAAATGTCTTGCTGTTGACATATTTAATGTTTTTAAATGTACAGA
 1750 1770 1790
 CATATTTAACTGGTGCACTTTGTAAATTCCTGGGGAAAACTTGCAGCTAAGGAGGGGAA

GenBank: F01666

FIGURE 4

1810 1830 1850
AAAAATGTTGTTTCCCTAATATCAAATGCAGTATATTTCTTCGTTCTTTTAAAGTTAATAG
1870 1890 1910
ATTTTTTTCAGACTTGTCAAGCCGTGTGCAAAAAAATTAAAAATGGATGCCTTGAATAATAAG
1930 1950 1970
CAGGATGTTGGCCACCAGGTGCCTTTCAAATTTAGAAACTAATTGACTTTTAGAAAGCTGA
1990 2010 2030
CATTGCCAAAAAGGATACATAATGGGCCACTGAAATCTGTCAAGAGTAGTTATATAATTG
2050 2070 2090
TTGAACAGGTGTTTTTCCACAAGTGCCGCAAATGTACCTTTTTTTTTTTTTTCAAAATAG
2110 2130 2150
AAAAGTTATTAGTGGTTTATCAGCAAAAAAGTCCAATTTTAATTTAGTAAATGTTATCTT
2170 2190 2210
ATACTGTACAATAAAAAACATTGCCTTTGAATGTTAATTTTTTGGTACAAAAATAAATTTA
2230 2250 2270
TATGAAAAAAAAAAAAAAGGGCGGCCGCTCTAGAGGGCCCTATTCTATAG

GenBank

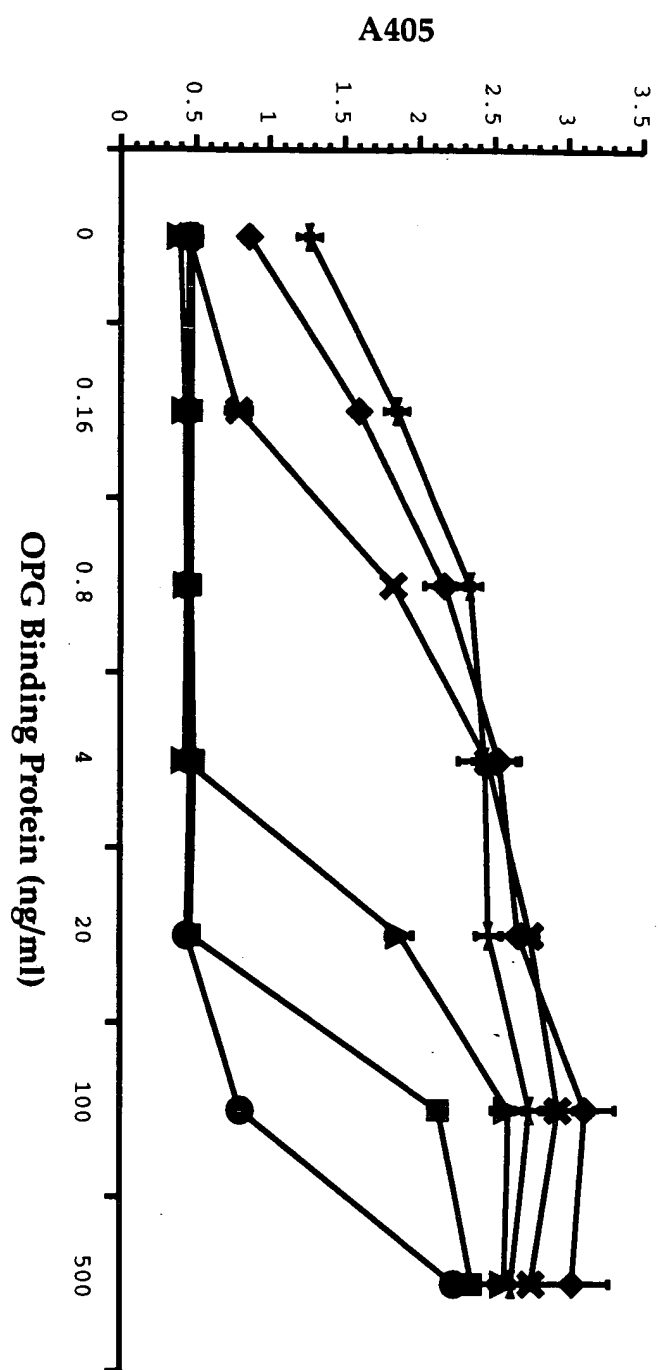
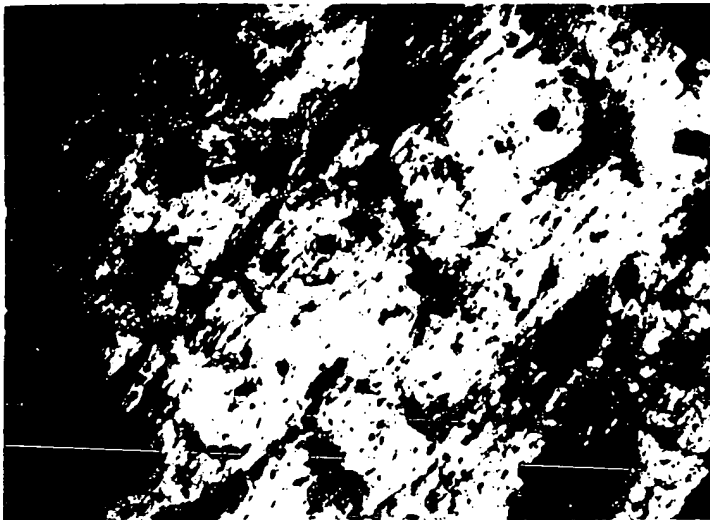
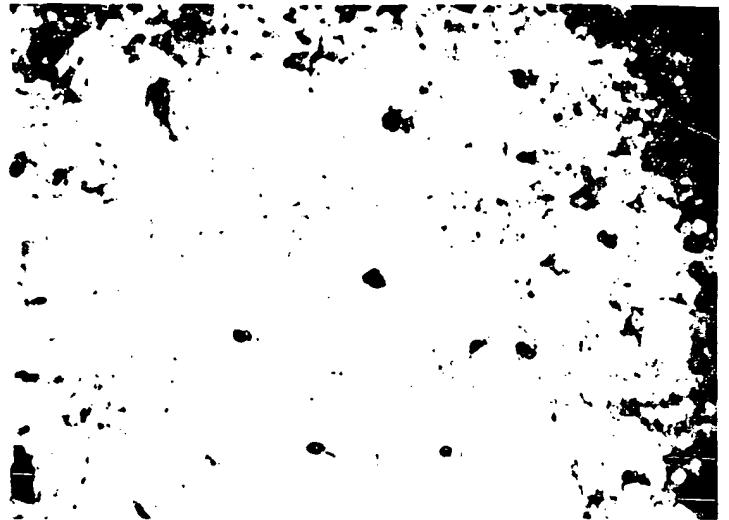


FIGURE 5

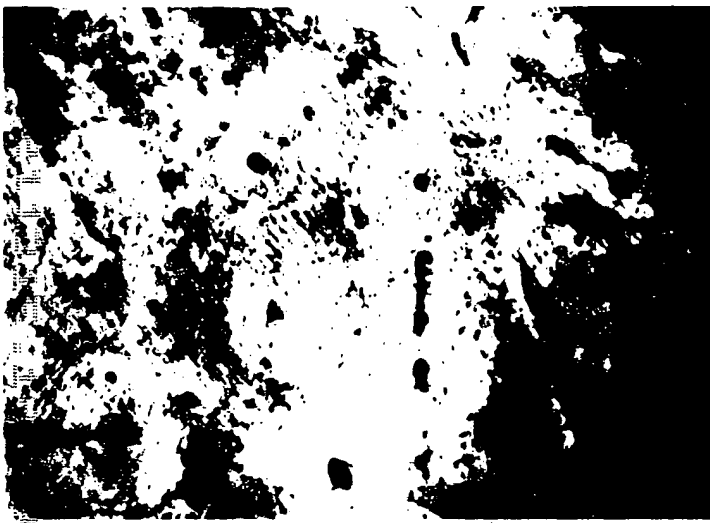
Toluidine Blue Staining



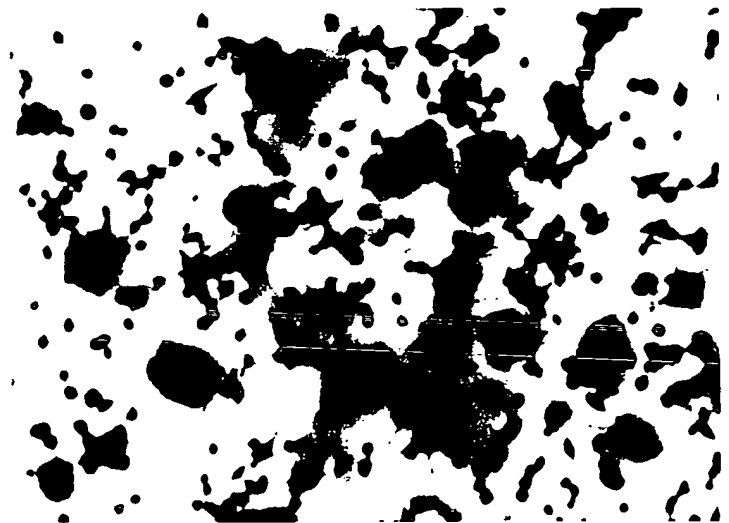
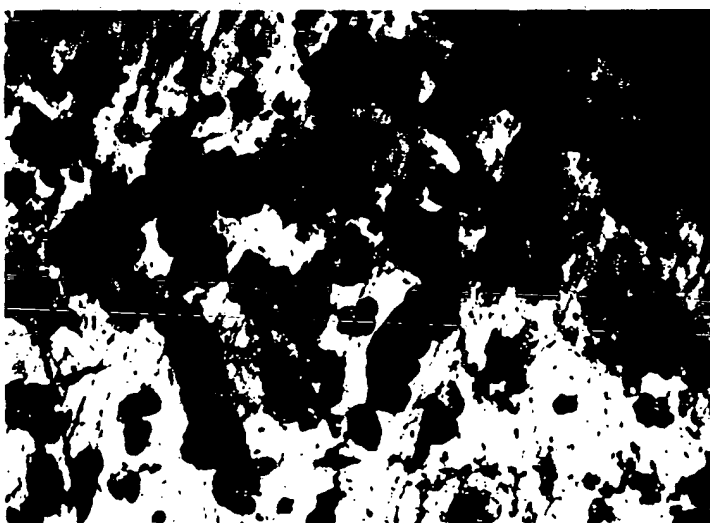
TRAP staining



Bone Marrow Cells + M-CSF-1



Bone Marrow Cells + OPG Binding Protein



Bone Marrow Cells + M-CSF-1 + OPG Binding Protein

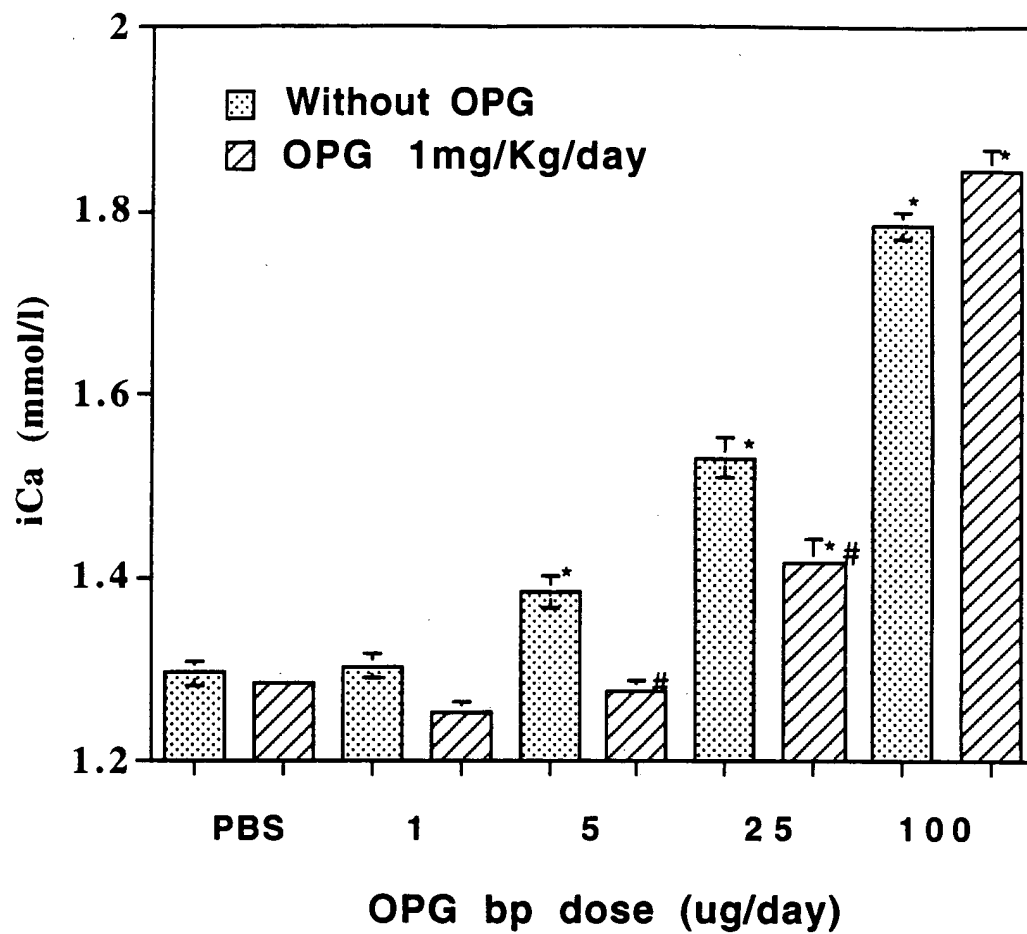
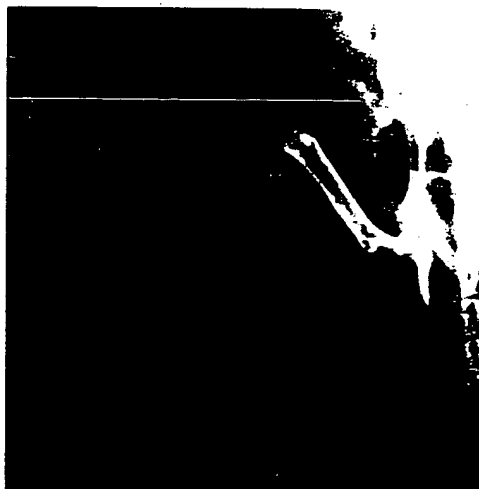


FIGURE 8

PBS



OPGbp 5ug/d



OPGbp 25ug/d



OPGbp100ug/d



FIGURE 9